# Using the underlying anatomy to infer white-matter pathways and vice versa

Anastasia Yendiki

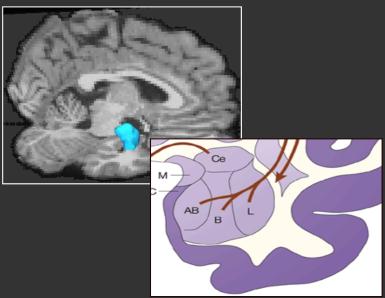


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# Tract-based amygdala segmentation

Work by Zeynep Saygin [zsaygin@mit.edu]

- Amygdala is important in
  - Fear conditioning
  - Emotional evaluation
  - Stimulus reappraisal
- Implicated in numerous pathologies
  - Depression
  - Anxiety disorders
  - Bipolar disorder
  - Autism



Baxter & Murray 2002

- Four nuclei with distinct functions described in animal studies
  - Central
  - Lateral
    - Basal & Accessory Basal
    - Medial
- Normal and pathological roles of nuclei unknown in humans

## Amygdaloid nuclei in MRI

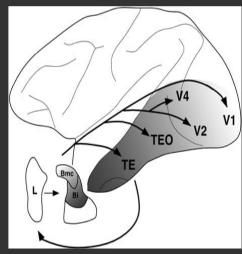
Work by Zeynep Saygin [zsaygin@mit.edu]

#### Structural MRI:

- Structural scan resolution and SNR too low to distinguish nuclei
- fMRI studies limited to averaging over entire amygdala
- Distinct but highly overlapping patterns of connectivity
  - Lateral and basal nuclei differentiated from central and medial by connectivity to visual areas
  - This is not enough to separate basal from lateral
- Connectivity patterns can be used to segment amygdala into nuclei



1mm<sup>3</sup> structural scan



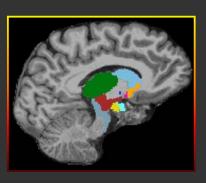
Freese & Amaral 2005

# Step 1: Anatomical ROIs

Work by Zeynep Saygin [zsaygin@mit.edu]



- 1mm iso 3D MPRAGE
- 3T, 32-channel head coil



Sub-cortical segmentation

- Seed: Amygdala
- Subcortical targets (18)



Cortical parcellation (surface-based)

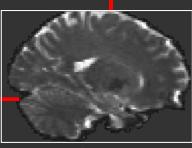
• Cortical targets (66)



84 targets
1 seed



Register DWI to MPRAGE



- 2mm iso DWI
- b = 1000
- 60 directions

## Step 2: Probabilistic tractography

Work by Zeynep Saygin [zsaygin@mit.edu]

• Calculate connection probability from each voxel in the amygdala to each target ROI

Amygdala

84 targets

voxels

Amygdala Voxel #	Brain Stem	RH Accumbens	RH Caudate	RH Putamen	RH Lateralorbitofrontal	RH Parahippocampal	RH Superiorfron
1	0.0274	0.1185	0.0877	0.0536	0.7915	0.0446	0.0192
2	0.0024	0.0040	0.0056	0.0000	0.0377	0.1293	0.0000
3	0.0091	0.0960	0.1154	0.0427	0.7338	0.0129	0.0142
4	0.0196	0.0258	0.0293	0.0216	0.3101	0.1956	0.0000
5	0.0021	0.0145	0.0136	0.0083	0.1165	0.1214	0.000
6	0.1642	0.0463	0.3096	0.1588	0.9952	0.0119	0.1077
7	0.0205	0.0043	0.0102	0.0032	0.0919	0.0108	0.0000
8	0.1458	0.0632	8080.0	0.0085	0.0761	0.0000	0.040
9	0.0475	0.0215	0.0443	0.0133	0.2313	0.0086	0.006
10	0.0391	0.1383	0.2337	0.0861	0.9736	0.0029	0.0360
11	0.0091	0.0293	0.0366	0.0129	0.8899	0.0003	0.0025
12	0.0031	0.0072	0.0073	0.0050	0.1411	0.0053	0.0015
13	0.1609	0.0196	0.0425	0.0245	0.2371	0.0000	0.0000
14	0.0188	0.1029	0.1106	0.0921	0.6792	0.0418	0.0161
15	0.030	0.0274	2 0275	0 17	0.065	25	2.0000

• The shold and binarize probability values

## Step 3: Classification

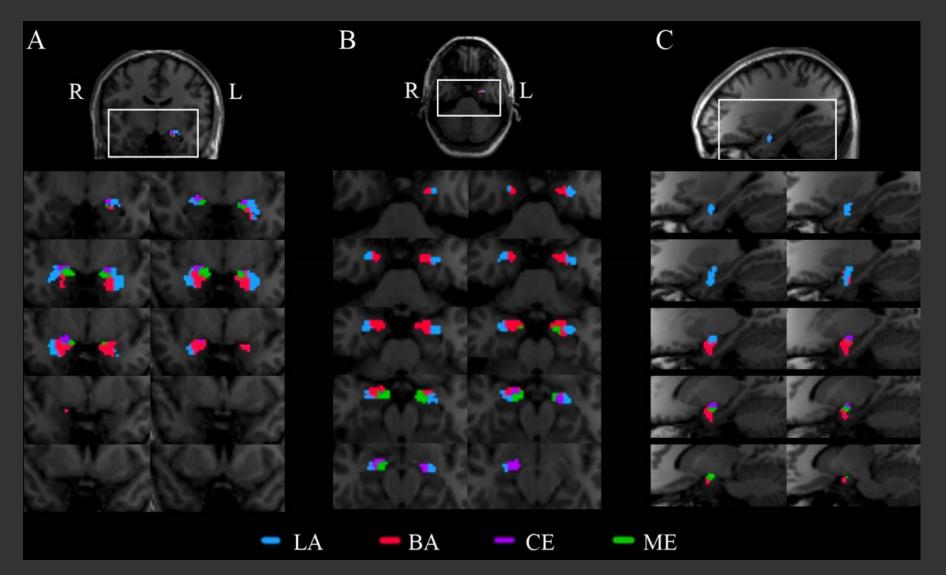
Work by Zeynep Saygin [zsaygin@mit.edu]

• Define nucleus groups based on summary of histological studies in rats, non-human primates, and humans

	rget combinations	Putative nucleus					
~(Superior parietal   Post-central <sup>1-4</sup>   Medial orbitofrontal <sup>1,2,5</sup>   Lateral occipital   Pericalcarine   Cuneus <sup>6</sup> ) & (Temporal pole   Fusiform   Lateral orbitofrontal & (Superior temporal   Inferior Temporal <sup>1-3,7-9</sup> )))							
(Parahippocampus & (Hippocampus 15,16   Rostral anterior cingulate 6,17   Lateral orbitofrontal   Medial orbitofrontal 18,2,3,5   Caudal middle-frontal   Lateral occipital   Pericalcarine   Cuneus   Lingual 6,19,20 ))   (Insula & (Accumbens   Superior frontal 6,21-23 ))							
~(Brain Stem <sup>10,11</sup> & Ventral Diencephalon <sup>6,12,13</sup> & Thalamus Proper <sup>14</sup> ) & (Ventral Diencephalon <sup>24,25</sup> & (Striatum <sup>5</sup>   Hippocampus <sup>15,16</sup> ))							
Brain Stem <sup>10,11</sup> & Ventral Diencephalon <sup>6,12,13</sup> & Thalamus Proper <sup>14</sup>							
	Table References						
1. (Aggleton et al., 1980) 2. (Stefanacci and Amaral, 2000) 3. (Stefanacci and Amaral, 2002) 4. (Turner et al., 1980) 5. (Gloor, 1994) 6. (Amaral and Price, 1984) 7. (Kosmal et al., 1997) 8. (Yukie, 2002) 9. (Bachevalier et al., 1997) 10. (Price and Amaral, 1981) 11. (Price, 1981) 12. (Amaral et al., 1982) 13. (Mehler, 1980)	14. (Amaral et al., 1992) 15. (Aggleton, 1986) 16. (Amaral, 1986) 17. (Vogt and Pandya, 1987) 18. (Carmichael and Price, 1995) 19. (Amaral et al., 2003) 20. (Freese and Amaral, 2005) 21. (Barbas and De Olmos, 1990) 22. (Ghashghaei and Barbas, 20 23. (Russchen et al., 1985) 24. (Price, 1986) 25. (Price et al., 1987)	9)					
~ NOT	Legend   OR & AND						

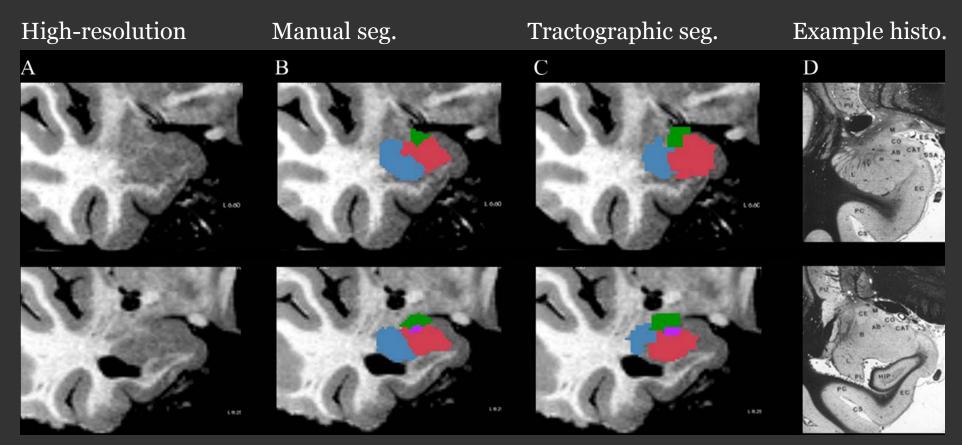
# Example subject

Work by Zeynep Saygin [zsaygin@mit.edu]



## Manual vs. tractographic segmentation

Work by Zeynep Saygin [zsaygin@mit.edu]

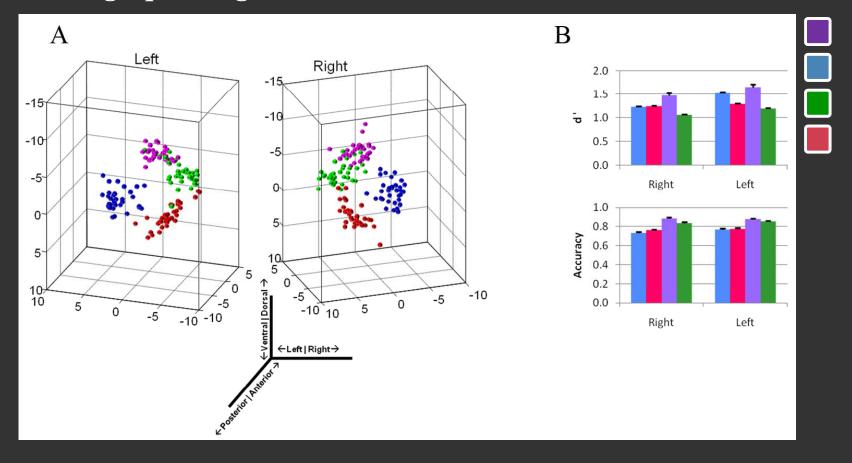


Dual-echo  $20^{0}$  flip angle  $TE_{0}/TE_{1}/TR = 5ms/12ms/20ms$  600µm isotropic 8 runs averaged  $\approx 2$  hrs

## Inter-subject consistency

Work by Zeynep Saygin [zsaygin@mit.edu]

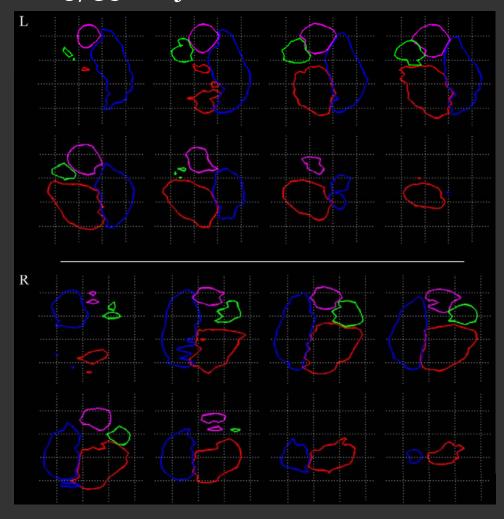
Tractographic segmentation results consistent across individuals



## Group probability maps

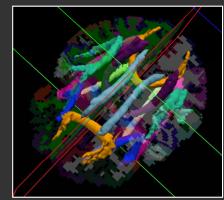
Work by Zeynep Saygin [zsaygin@mit.edu]

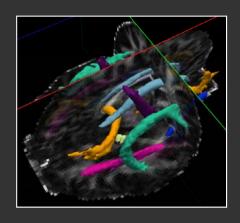
Group probability maps of tractographic segmentation labels, thresholded at >= 15/35 subjects



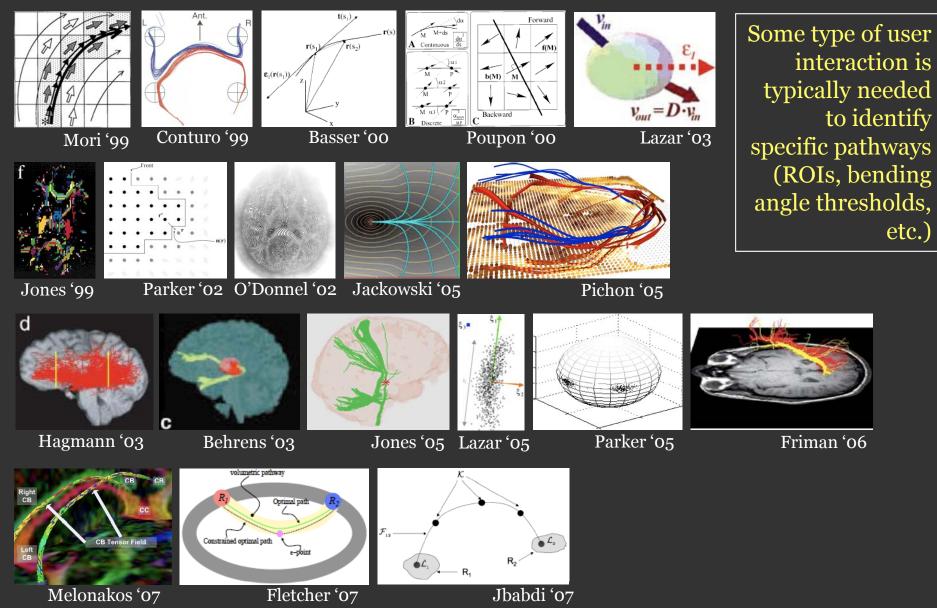
# Automated tractography

- TRActs Constrained by UnderLying Anatomy (TRACULA)
- Automatic reconstruction of probabilistic distributions of 18 major white-matter pathways
- No manual labeling of ROIs needed
- Use prior information on pathway anatomy from training data:
  - Manually labeled pathways in training subjects
  - FreeSurfer segmentations of same subjects
  - Learn neighboring anatomical labels along pathway
- Beta version available in FreeSurfer 5.1

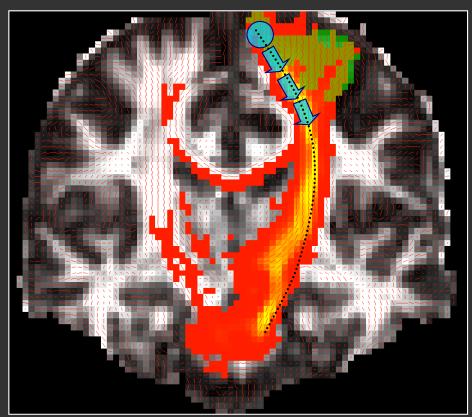


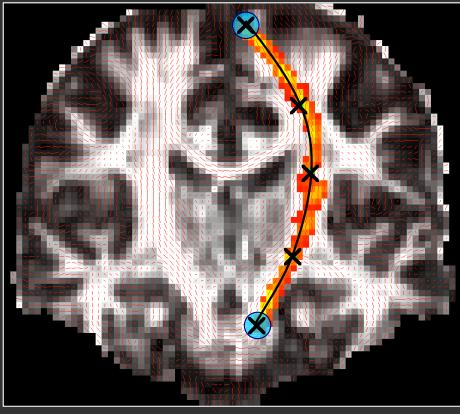


# Many options for tractography!



## Local vs. global tractography





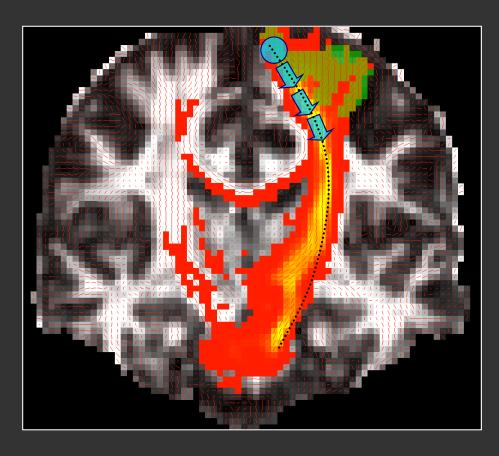
#### Local tractography:

Fits pathway step-by-step, using local diffusion orientation at each step

#### Global tractography:

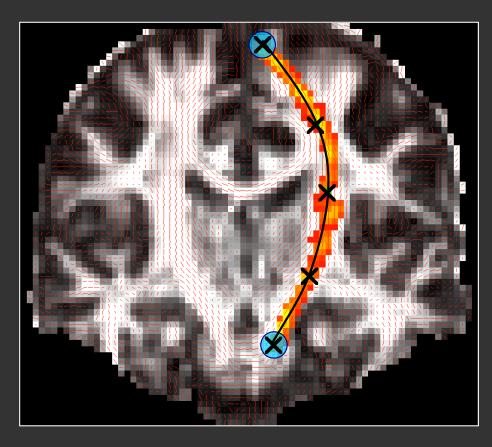
Fits the entire pathway, using diffusion orientation at all voxels along pathway length

# Local tractography



- Best suited for exploratory study of connections
- All connections from a seed region, not constrained to a specific target region
- How do we isolate a specific white-matter pathway?
  - Thresholding?
  - Intermediate ROIs?
- Non-dominant connections are hard to reconstruct
- Results are not symmetric between "seed" and "target" regions
- Sensitive to areas of high local uncertainty in orientation (*e.g.*, pathaway crossings), errors propagate from those areas

## Global tractography

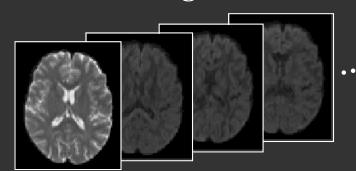


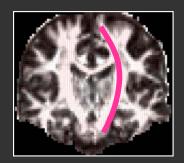
- Best suited for reconstruction of known white-matter pathways
- Constrained to connection of two specific end regions
- Not sensitive to areas of high local uncertainty in orientation, integrates over entire pathway
- Symmetric between "seed" and "target" regions
- Need to search through a large solution space of all possible connections between two regions:
  - Computationally expensive
  - Sensitive to initialization

# Global probabilistic tractography

Have image data **Y** 

Want most probable path F





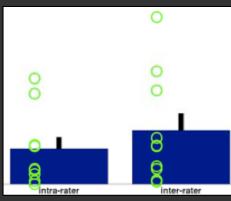
- Determine the most probable path based on:
  - What the images tell us about the path
  - What we already know about the path
- Estimate posterior probability of path F given images Y

$$p(F \mid Y) / p(Y \mid F) \notin p(F)$$

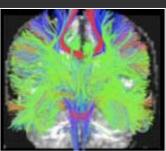
- p(Y | F): Uncertainty due to imaging noise
   Fit of pathway orientation to ball-and-stick model parameters
   [Behrens '03, Jbabdi '07]
- -p(F): Uncertainty due to anatomical variability Fit of pathway to prior anatomical knowledge from training set

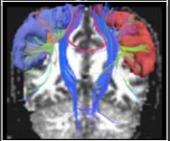
## White-matter pathway atlas

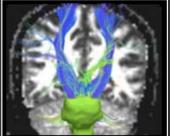
- Labeling based on an established protocol [Wakana '07]
- Corticospinal tract
- Inferior longitudinal fasciculus
- Uncinate fasciculus
- Corpus callosum
  - Forceps major
  - Forceps minor
- Anterior thalamic radiation
- Cingulum
  - Cingulate (supracallosal)
  - Angular (infracallosal)
- Superior longitudinal fasciculus
  - Parietal
  - Temporal

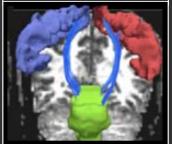


Intra/inter-rater errors: 1mm/2mm on average



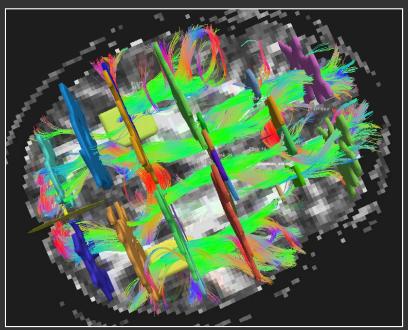


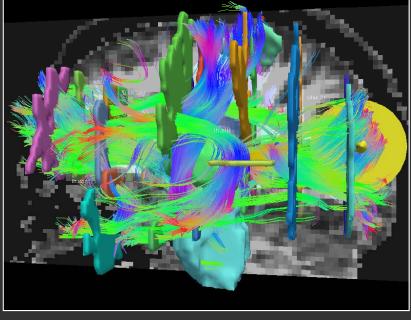




## White-matter pathway atlas

• Manual labeling of paths in training subjects performed in Trackvis



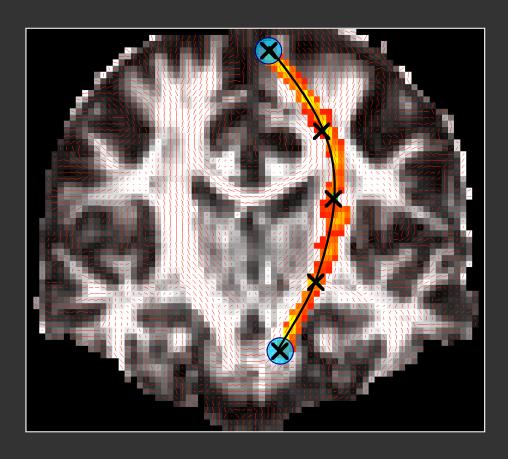


• Anatomical segmentation maps of training subjects from FreeSurfer





### TRACULA outputs

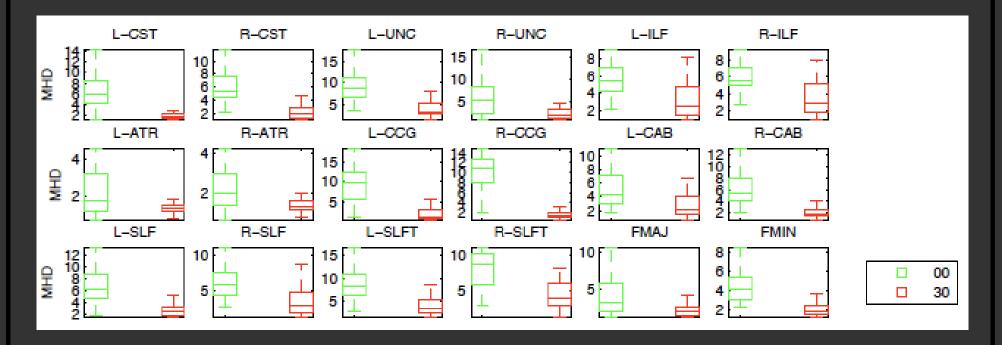


- Reconstruction outputs:
  - Posterior probability distribution of pathway given data (3D)
  - Maximum *a posteriori* (MAP)pathway (1D)
- Tract-based diffusion measures (FA, MD, RD, AD, etc):
  - Average over pathway distribution
  - Weighted average over pathway distribution
  - Average over MAP pathway
  - As a function of arc length along MAP pathway

## Reliability in healthy subjects

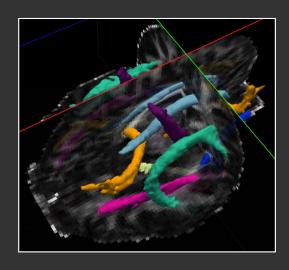
Data courtesy of Dr. Randy Gollub and MIND Institute

- Reconstruct pathways in 9 healthy subjects' test-retest data with
  - No training subjects
  - 30 of the remaining healthy subjects as training data
- Evaluate distance b/w automatically reconstructed MAP pathway from the test and retest scan

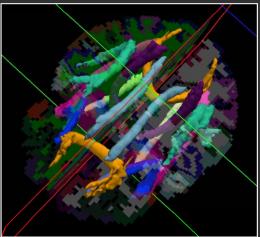


## Schizophrenia study

Data courtesy of Dr. Randy Gollub and MIND Institute



QuickTime™ and a H.264 decompressor are needed to see this picture.

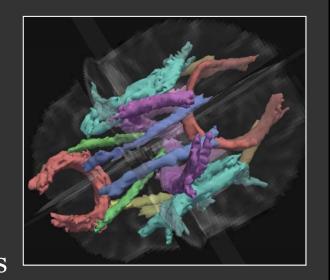


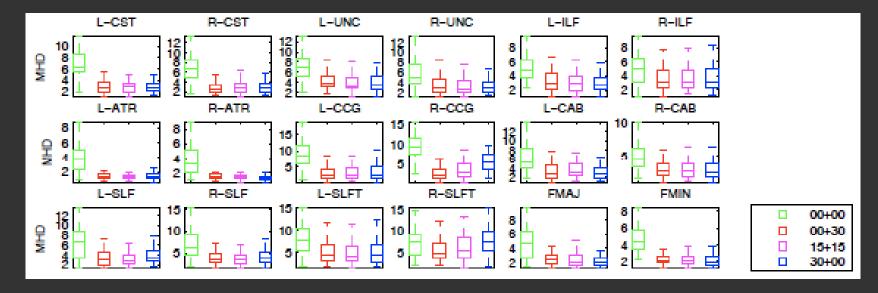
Pathway distributions reconstructed automatically in a SZ patient using 30 healthy training subjects

# Schizophrenia study

Data courtesy of Dr. Randy Gollub and MIND Institute

- Reconstruct pathways in 34 SZ patients and 23 healthy controls with
  - No training subjects
  - 30 healthy training subjects
  - 15 healthy / 15 SZ training subjects
  - 30 SZ training subjects
- Evaluate distance b/w automatically reconstructed and manually labeled pathways





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- Zeynep Saygin





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- The MIND Institute